

B1  
determining the methylation of cytosine residue(s) at the specific region of epidermal growth factor receptor and,  
detecting a psoriasis patient whose sample's genomic DNA has less cytosine residues than healthy person's genomic DNA.

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- B2
5. A diagnostic method of claim 1 wherein the specific region is a region in CpG island of promoter or intron.
6. A diagnostic method of claim 1 wherein the specific region is a region involved in the expression of epidermal growth factor receptor gene and a region represented by the nucleotide sequence from 381<sup>st</sup> position to 962<sup>nd</sup> position in the nucleotide sequence as described in Seq. ID No. 4.
7. A diagnostic method of claim 1 characterized by determining the methylation of cytosine of residue 668, residue 671, residue 687 and residue 697 in the nucleotide sequence as described in Seq. ID No. 4.
8. A diagnostic method of claim 1 characterized by determining the methylation of cytosine-residues of 668<sup>th</sup> in the nucleotide sequence as described in Seq. ID No. 4.
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- B3
11. A diagnostic method of claim 10 characterized by determining the level of methylation of 268<sup>th</sup>, 276<sup>th</sup> and 288<sup>th</sup> cytosine residues in the nucleotide sequence as described in Seq. ID No. 8.
12. A diagnostic method of claim 11 characterized by analyzing the level of methylation of 268<sup>th</sup> cytosine residue in the nucleotide sequence as described in Seq. ID No. 8.
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- B4
15. A method of detecting the methylation of cytosine residue(s) in the specific region of DNA involved in the expression of epidermal growth factor receptor gene isolated sampling-blood.